RAW SEQUENCE LISTING

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Application Serial Number: _10/544,180_

Source: _PCT/lo_

Date Processed by STIC: _8/11/05_

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PCT

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RAW SEQUENCE LISTING                    DATE: 08/11/2005
PATENT APPLICATION:  US/10/544,180      TIME: 13:36:16

Input Set : A:\14-03 US.ST25.txt
Output Set: N:\CRF4\08112005\J544180.raw
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 3 <110> APPLICANT: Mohnen, Debra
 4        Sterling, Jason D.
 5        Doong, Ron L.
 6        Kolli, Venkata S.K.
 7        Hahn, Michael G.
 9 <120> TITLE OF INVENTION: Galacturonosyltransferases, nucleic acids encoding same, and
uses
10        therefor
12 <130> FILE REFERENCE: 14-03 US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/544,180
15 <141> CURRENT FILING DATE: 2005-08-02
17 <150> PRIOR APPLICATION NUMBER: PCT/US2004/003545
18 <151> PRIOR FILING DATE: 2004-02-05
20 <150> PRIOR APPLICATION NUMBER: US 60/445,539
21 <151> PRIOR FILING DATE: 2003-02-06
23 <160> NUMBER OF SEQ ID NOS: 50
25 <170> SOFTWARE: PatentIn version 3.2
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2022
29 <212> TYPE: DNA
30 <213> ORGANISM: Arabidopsis thaliana
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37 ggccgaggag tgtatatcga ttcctcaaat gattattcaa ttgtttctgt gaagcagaat     180
39 cttgactgga gagaacgttt agcaatgcaa tctgttagat ctctttttctc gaaagagata    240
41 ctagatgtta tagcaaccag cacagctgat ttgggtcctc ttagccttga ttctttttaag    300
43 aaaaacaatt tgtctgcatc atggcgggga accggagtag acccctcctt tagacattct     360
45 gagaatccag caactcctga tgtcaaatct aataacctga atgaaaaacg tgacagcatt     420
47 tcaaaagata gtatccatca gaaagttgag acacctacaa agattcacag aaggcaacta     480
49 agagagaaaa ggcgtgagat gcgggcaaat gagttagttc agcacaatga tgacacgatt     540
51 ttgaaactcg aaaatgctgc cattgaacgc tctaagtctg ttgattctgc agtccttggt     600
53 aaatacagta tttggagaag agaaaatgag aatgacaact ctgattcaaa tatacgcttg     660
55 atgcgggatc aagtaataat ggctagagtc tatagtggga ttgcaaaatt gaaaaacaag     720
57 aacgatttgt tacaagaact ccaggcccga cttaaggaca gccaacgggt tttgggggaa     780
59 gcaacatctg atgctgatct tcctcggagt gcgcatgaga aactcagagc catgggtcaa     840
61 gtcttggcta aagctaagat gcagttatat gactgcaagc tggttactgg aaagctgaga     900
63 gcaatgcttc agactgccga cgaacaagtg aggagcttaa agaagcagag tacttttctg     960
65 gctcagttag cagcaaaaac cattccaaat cctatccatt gcctatcaat gcgcttgact    1020
67 atcgattact atcttctgtc tccggagaaa agaaaattcc ctcggagtga aaacctagaa    1080
69 aaccctaatc tttatcatta tgccctcttt tccgacaatg tattagctgc atcagtagtt    1140
71 gttaactcaa ccatcatgaa tgccaaggat ccttctaagc atgttttttca ccttgtcacg    1200
73 gataaactca atttcggagc aatgaacatg tggttcctcc taaacccacc cggaaaggca    1260
75 accatacatg tggaaaacgt cgatgagttt aagtggctca attcatctta ctgtcctgtc    1320
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77 cttcgtcagc ttgaatctgc agcaatgaga gagtactatt ttaaagcaga ccatccaact   1380
79 tcaggctctt cgaatctaaa atacagaaac ccaaagtatc tatccatgtt gaatcacttg   1440
81 agattctacc tccctgaggt ttatcccaag ctgaacaaaa tcctcttcct ggacgatgac   1500
83 atcattgttc agaaagactt gactccactc tgggaagtta acctgaacgg caaagtcaac   1560
85 ggtgcagtcg aaacctgtgg ggaaagtttc cacagattcg acaagtatct caacttttcg   1620
87 aatcctcaca ttgcgaggaa cttcaatcca aatgcttgtg atgggctta tggaatgaac    1680
89 atgttcgacc taaaggaatg gaagaagaga gacatcactg gtatatacca caagtggcaa   1740
91 aacatgaatg agaacaggac actatggaag ctagggacat gccaccagg attaataaca    1800
93 ttctacggat taacacatcc cttaaacaag gcgtggcatg tgctgggact tggatataac   1860
95 ccgagtatcg acaagaagga cattgagaat gcagcagtgg ttcactataa cgggaacatg   1920
97 aaaccatggt tggagttggc aatgtccaaa tatcggccgt attggaccaa gtacatcaag   1980
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105 <213> ORGANISM: Arabidopsis thaliana
107 <400> SEQUENCE: 2
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114                 20                  25                  30
117 Phe Ala Pro Leu Cys Phe Phe Val Gly Arg Gly Val Tyr Ile Asp Ser
118             35                  40                  45
121 Ser Asn Asp Tyr Ser Ile Val Ser Val Lys Gln Asn Leu Asp Trp Arg
122         50                  55                  60
125 Glu Arg Leu Ala Met Gln Ser Val Arg Ser Leu Phe Ser Lys Glu Ile
126 65                  70                  75                  80
129 Leu Asp Val Ile Ala Thr Ser Thr Ala Asp Leu Gly Pro Leu Ser Leu
130                 85                  90                  95
133 Asp Ser Phe Lys Lys Asn Asn Leu Ser Ala Ser Trp Arg Gly Thr Gly
134                 100                 105                 110
137 Val Asp Pro Ser Phe Arg His Ser Glu Asn Pro Ala Thr Pro Asp Val
138             115                 120                 125
141 Lys Ser Asn Asn Leu Asn Glu Lys Arg Asp Ser Ile Ser Lys Asp Ser
142         130                 135                 140
145 Ile His Gln Lys Val Glu Thr Pro Thr Lys Ile His Arg Arg Gln Leu
146 145                 150                 155                 160
149 Arg Glu Lys Arg Arg Glu Met Arg Ala Asn Glu Leu Val Gln His Asn
150                 165                 170                 175
153 Asp Asp Thr Ile Leu Lys Leu Glu Asn Ala Ala Ile Glu Arg Ser Lys
154             180                 185                 190
157 Ser Val Asp Ser Ala Val Leu Gly Lys Tyr Ser Ile Trp Arg Arg Glu
158         195                 200                 205
161 Asn Glu Asn Asp Asn Ser Asp Ser Asn Ile Arg Leu Met Arg Asp Gln
162         210                 215                 220
165 Val Ile Met Ala Arg Val Tyr Ser Gly Ile Ala Lys Leu Lys Asn Lys
166 225                 230                 235                 240
169 Asn Asp Leu Leu Gln Glu Leu Gln Ala Arg Leu Lys Asp Ser Gln Arg
170             245                 250                 255
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Input Set : A:\14-03 US.ST25.txt
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177 Glu Lys Leu Arg Ala Met Gly Gln Val Leu Ala Lys Ala Lys Met Gln
178         275                 280                 285
181 Leu Tyr Asp Cys Lys Leu Val Thr Gly Lys Leu Arg Ala Met Leu Gln
182         290                 295                 300
185 Thr Ala Asp Glu Gln Val Arg Ser Leu Lys Lys Gln Ser Thr Phe Leu
186 305                 310                 315                 320
189 Ala Gln Leu Ala Ala Lys Thr Ile Pro Asn Pro Ile His Cys Leu Ser
190                 325                 330                 335
193 Met Arg Leu Thr Ile Asp Tyr Tyr Leu Leu Ser Pro Glu Lys Arg Lys
194         340                 345                 350
197 Phe Pro Arg Ser Glu Asn Leu Glu Asn Pro Asn Leu Tyr His Tyr Ala
198         355                 360                 365
201 Leu Phe Ser Asp Asn Val Leu Ala Ala Ser Val Val Val Asn Ser Thr
202     370                 375                 380
205 Ile Met Asn Ala Lys Asp Pro Ser Lys His Val Phe His Leu Val Thr
206 385                 390                 395                 400
209 Asp Lys Leu Asn Phe Gly Ala Met Asn Met Trp Phe Leu Leu Asn Pro
210                 405                 410                 415
213 Pro Gly Lys Ala Thr Ile His Val Glu Asn Val Asp Glu Phe Lys Trp
214         420                 425                 430
217 Leu Asn Ser Ser Tyr Cys Pro Val Leu Arg Gln Leu Glu Ser Ala Ala
218         435                 440                 445
221 Met Arg Glu Tyr Tyr Phe Lys Ala Asp His Pro Thr Ser Gly Ser Ser
222     450                 455                 460
225 Asn Leu Lys Tyr Arg Asn Pro Lys Tyr Leu Ser Met Leu Asn His Leu
226 465                 470                 475                 480
229 Arg Phe Tyr Leu Pro Glu Val Tyr Pro Lys Leu Asn Lys Ile Leu Phe
230                 485                 490                 495
233 Leu Asp Asp Asp Ile Ile Val Gln Lys Asp Leu Thr Pro Leu Trp Glu
234         500                 505                 510
237 Val Asn Leu Asn Gly Lys Val Asn Gly Ala Val Glu Thr Cys Gly Glu
238         515                 520                 525
241 Ser Phe His Arg Phe Asp Lys Tyr Leu Asn Phe Ser Asn Pro His Ile
242     530                 535                 540
245 Ala Arg Asn Phe Asn Pro Asn Ala Cys Gly Trp Ala Tyr Gly Met Asn
246 545                 550                 555                 560
249 Met Phe Asp Leu Lys Glu Trp Lys Lys Arg Asp Ile Thr Gly Ile Tyr
250                 565                 570                 575
253 His Lys Trp Gln Asn Met Asn Glu Asn Arg Thr Leu Trp Lys Leu Gly
254         580                 585                 590
257 Thr Leu Pro Pro Gly Leu Ile Thr Phe Tyr Gly Leu Thr His Pro Leu
258         595                 600                 605
261 Asn Lys Ala Trp His Val Leu Gly Leu Gly Tyr Asn Pro Ser Ile Asp
262     610                 615                 620
265 Lys Lys Asp Ile Glu Asn Ala Ala Val Val His Tyr Asn Gly Asn Met
266 625                 630                 635                 640
269 Lys Pro Trp Leu Glu Leu Ala Met Ser Lys Tyr Arg Pro Tyr Trp Thr
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282 <211> LENGTH: 1860
283 <212> TYPE: DNA
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286 <400> SEQUENCE: 3
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291 ctcggtcttc acaatggctt tcactctcct ggatttgtca ctgttcaacc ggcttcttca   180
293 tttgagagct ttaccagaat caatgctact aagcatacac agagagatgt atccgaacgg   240
295 gtcgatgagg ttcttcaaaa aatcaatcca gttcttccca agaaaagcga cataaacgtg   300
297 ggttccagag atgtgaatgc aacaagcggc actgattcta aaaaaagagg attaccagtg   360
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305 aagcaaatga aggaccagct gtttgtggct agagcatact atcccagtat tgctaaaatg   600
307 ccttctcaaa gcaagttgac tcgggatatg aaacagaata tccaagagtt tgagcgtatt   660
309 cttagtgaaa gttctcaaga tgctgacctt ccaccacagg ttgataaaaa gttgcagaag   720
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313 aaattgagac agatccttga tttgactgag gatgaagcta gtttccacat gaaacagagt   840
315 gtgttcctct accagcttgc agtacagaca atgcctaaga gtcttcattg cttgtcaatg   900
317 cgactaactg tggaacattt caagtcagat tcacttgagg atcccattag tgagaaattt   960
319 tcagatccct cattacttca ctttgttatc atctccgata atatactagc atcgtccgtt  1020
321 gtgatcaact caacggttgt acatgcaagg gacagtaaaa actttgtttt ccatgtactg  1080
323 acagacgagc agaattactt tgcaatgaaa caatggttta ttaggaatcc ttgcaaacaa  1140
325 tcaactgttc aagtattgaa cattgaaaaa ctcgagctgg acgattctga tatgaaactg  1200
327 tctttgtctg cggagttccg tgtttccttc cccagtggtg acctttttggc gtctcaacag  1260
329 aatagaacac actacttatc cctttttctct caatctcact atcttcttcc caaattattt  1320
331 gacaaattgg agaaggttgt gattctggat gatgacgttg tagtccagcg agacttatct  1380
333 cccctttggg accttgatat ggaagggaaa gtgaatggcg ctgttaagtc gtgcactgtg  1440
335 agattgggtc agctaaggag tctcaagaga ggaaattttg ataccaatgc ttgtctctgg  1500
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351 <211> LENGTH: 619
352 <212> TYPE: PRT
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361 Arg Trp Lys Val Leu Val Ile Gly Val Leu Val Leu Val Ile Leu Ser
362             20                  25                  30
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365 Met Leu Val Pro Leu Ala Phe Leu Leu Gly Leu His Asn Gly Phe His
366         35                  40                  45
369 Ser Pro Gly Phe Val Thr Val Gln Pro Ala Ser Ser Phe Glu Ser Phe
370         50                  55                  60
373 Thr Arg Ile Asn Ala Thr Lys His Thr Gln Arg Asp Val Ser Glu Arg
374 65                  70                  75                  80
377 Val Asp Glu Val Leu Gln Lys Ile Asn Pro Val Leu Pro Lys Lys Ser
378                 85                  90                  95
381 Asp Ile Asn Val Gly Ser Arg Asp Val Asn Ala Thr Ser Gly Thr Asp
382                 100                 105                 110
385 Ser Lys Lys Arg Gly Leu Pro Val Ser Pro Thr Val Val Ala Asn Pro
386         115                 120                 125
389 Ser Pro Ala Asn Lys Thr Lys Ser Glu Ala Ser Tyr Thr Gly Val Gln
390         130                 135                 140
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394 145                 150         155                 160
397 Tyr Gly Ser Tyr Cys Leu Trp Arg Glu Glu Asn Lys Glu Pro Met Lys
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401 Asp Ala Lys Val Lys Gln Met Lys Asp Gln Leu Phe Val Ala Arg Ala
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405 Tyr Tyr Pro Ser Ile Ala Lys Met Pro Ser Gln Ser Lys Leu Thr Arg
406         195                 200                 205
409 Asp Met Lys Gln Asn Ile Gln Glu Phe Glu Arg Ile Leu Ser Glu Ser
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413 Ser Gln Asp Ala Asp Leu Pro Pro Gln Val Asp Lys Lys Leu Gln Lys
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434 305                 310                 315                 320
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446         355                 360                 365
449 Met Lys Gln Trp Phe Ile Arg Asn Pro Cys Lys Gln Ser Thr Val Gln
450     370                 375                 380
453 Val Leu Asn Ile Glu Lys Leu Glu Leu Asp Asp Ser Asp Met Lys Leu
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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number